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Segregation of vegetative and reproductive traits associated with tuber yield and quality in water yam (*Dioscorea alata* L.)

Alieu Sartie[1,2*] and Robert Asiedu[2]

[1]AgResearch Ltd., Grasslands Research Centre, Private Bag 11008, Palmerston North 4442, New Zealand.
[2]International Institute of Tropical Agriculture (IITA), c/o IITA Limited, Carolyn House, 26 Dingwall Rd, Croydon CR9 3EE, UK.

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Water yam (*Dioscorea alata* L.) is an important source of food for millions of people in Africa, Asia, South America, Caribbean and the South Pacific islands. Genetic mapping populations of this species have been produced as part of efforts to raise the efficiency of breeding through development and use of molecular markers. In this study, an F_1 mapping population (AM1) of *D. alata*, exhibited segregation for both tuber yield- and quality- related traits when evaluated in the field for 12 agronomic characters: days to shoot emergence, number of primary vines per plant, days to flowering, flower sex, flowering intensity, days to tuber initiation, number of tubers per plant, tuber yield per plant, tuber shape, bulbil formation, tuber browning and reaction to anthracnose (*Colletotrichum gloeosporioides* Penz) infection. The number of tubers/plant and the number of primary vines/plant were moderately positively correlated, while most of the other quantitative traits were weakly correlated with each other. There were more males (49%) than females (19.9%) identified in the population, however more than a quarter of the population (31%) did not flower and their sexes could not be determined. 20% of the progeny was resistant or tolerant to field infection by anthracnose. Population AM1 will be a valuable resource as a mapping population for genetic analysis and molecular marker development for tuber quality and several other agronomic traits in *D. alata*.

Key words: Flowering intensity, marker assisted breeding, mapping population, phenotypic variation and trait segregation, tuber yield and quality, water yam.

INTRODUCTION

Yam (genus *Dioscorea* in family Dioscoreaceae) is a polyploid and clonally-propagated crop that is cultivated for its starchy tubers. It is an important source of food and income for over 300 million people in Africa, Asia, South America, Caribbean and the South Pacific islands (Degras, 1983). It also has considerable socio-cultural significance, especially in West Africa and the South Pacific islands, where it is central to important annual ceremonies. Although there are more than 600 species of yam, only ten are generally cultivated for food including:

*Corresponding author. E-mail: sartiealieu@hotmail.com. Tel: +64 6 3588018 / +64 6 2108209408.

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Table 1. List of qualitatively scored traits assessed by using subjective scale during vegetative and reproduction growth and after harvest of *D. alata* mapping population AM1 and the two parents during 2010/2011 yam growing season at IITA, Ibadan, Nigeria. The assessment was performed in accordance with the IPGRI/IITA descriptors for yam.

Trait	Score code-descriptor state
Flower sex	Male = 1; Female = 2; Monoecious = 3; None = 4
Flowering Intensity	Very high flowering = 1; Moderate = 2; Scattered / Few = 3; None = 4
Tuber shape	Round = 1; Oval = 2; Oval-oblong = 3; Cylindrical = 4; Flattened = 5
Bulbil formation	High (>10 bulbils) = 1; Moderate = (6-10) = 2; Low (1-5) = 3; None = 4
Tuber oxidation	No oxidation = 0; Fast oxidation = 1; Slow oxidation = 2
Reaction to Anthracnose disease	Healthy (<2% or no symptom) = 1; Slightly infected (2-25% symptom) =2; Highly infected (>25% symptom) = 3

Dioscorea alata L. (water yam, greater yam), *D. rotundata* Poir. (white yam, white guinea yam) and *D. cayenensis* Lam. (yellow yam, yellow guinea yam) (Lebot, 2009).

D. alata was introduced to Africa from Asia during the 16th century (Hahn, 1995) and is the most widely distributed *Dioscorea* species in the tropics. It features high yield potential, ease of propagation (through production of bulbils and reliability of sprouting), early growth vigour for weed suppression and long storability of tubers. Although these characteristics are valuable for economic production, the species has major limitations in the field; including high susceptibility of most varieties to the devastating foliar disease, anthracnose caused by *Colletotrichum gloeosporioides* Penz, tendency towards poor or non-flowering, lack of synchrony in flowering of male and female genotypes and variation in flowering intensity with season and location (Hamadina et al., 2009). Tuber browning, caused by an enzyme catalysed oxidative reaction whereby a cut surface turns brown on exposure to air, is a problem in *D. alata* and other yam species (Martin and Ruberte, 1976), affecting their eating quality. Analysis of tuber yield-related traits in eight accessions of *D. alata,* comprising five breeding lines and three landrace varieties identified shoot dry weight and time of shoot emergence as traits related to fresh tuber yield (Sartie et al., 2011). Shoot dry weight had the strongest positive effect, while time of shoot emergence had a negative effect.

As genetic improvement of yam through conventional breeding alone is difficult and slow, efforts are being made to introduce marker-assisted selection to improve the efficiency of yam breeding programmes. Molecular markers, including simple sequence repeats (SSRs) and single nucleotide polymorphism (SNPs) are being developed (Satya et al., 2011; Bhattacharjee et al., 2013; Tamiru et al., 2013) for the purpose of screening genetic mapping populations segregating for key traits of interest and identifying markers linked to those traits for use as aids in selection by breeders. As a previous F_1 mapping population deve-loped for *D. alata* (Mignouna et al., 2002) has been lost, new mapping populations have recently been developed from breeding germplasm at the International Institute of Tropical Agriculture (IITA) for marker discovery in *D. alata* and *D. rotundata* (Sartie and Asiedu, 2011).

The aim of this research was to evaluate a *D. alata* L. genetic mapping population for phenotypic variation in vegetative and reproductive traits associated with tuber yield, tuber quality and anthracnose disease resistance.

MATERIALS AND METHODS

Yam genotypes and experimental design

Seventy eight (78) out of 144 genotypes from the genetic mapping population AM1 (Sartie and Asiedu, 2011) and the two parents were assessed in the field from planting to tuber harvest during the 2010/2011 yam growing season at IITA, Ibadan, Nigeria. Population AM1 is an F_1 full-sib population developed from crossing *Dioscorea alata* L. accessions TDa 01/00081 and TDa 87/01091, which differ in breeding traits of interest. For each genotype, 6 to 15 tuber setts weighing 600 g were prepared and buried in carbonized rice husks for sprouting. The sprouted setts were transplanted into mounds (about 30 cm high) in the field at a spacing of 0.5 m × 1 m in α-lattice design with two replications of three plants per genotype in April 2010. The remaining setts and the 66 genotypes that had less than 5 setts were planted at the borders of the experiment for tuber multiplication. Harvest was in February 2011.

Trait phenotyping

Twelve agronomic traits were assessed: days to shoot emergence, number of primary vines per plant, days to tuber initiation, days to flowering, flowering intensity, flowering sex, number of tubers per plant, tuber yield per plant, tuber shape, tuber oxidation, bulbil formation, and reaction to anthracnose infection. Of these, six traits (Table 1): flowering intensity, flowering sex, bulbil formation, tuber shape, tuber oxidation and reaction to anthracnose infection were scored using qualitative (subjective) scales, following the internationally agreed descriptor list for yam (IPGRI/IITA, 1997). Tuber oxidation was scored by visual observation of tuber parenchyma 2 min after cutting the fresh tuber, and was performed at the time of preparation of setts for planting each genotype. Anthracnose resistance phenotyping involved scoring for both the minimum and maximum symptoms observed on a naturally infected plant on the field. Days to shoot emergence, number of primary vines per plant, days to tuber initiation, days to flowering, number of tubers per plant, and tuber yield per plant were scored quantitatively as follows:

Days to shoot emergence

This was recorded as the number of days between the planting of a

Table 2. Phenotype of parents and progeny of 6 qualitatively scored traits assessed in mapping population AM1 in 2010/2011 yam growing season. Phenotypic proportion was calculated as percentage of setts from progeny and two parental lines in each qualitative trait category.

Qualitatively scored trait	Parental phenotype		Progeny phenotype
	TDa 01/00081 (♀)	TDa 87/01091 (♂)	Phenotype
Flowering sex	Female (50%), None (50%)	Male (66.7%), None (31.0%)	Male (49.0%), None (31.0%), Female (19.9%)
Flowering intensity	Very high (60.0%), None (40%)	Scattered/few (66.7%), None (33.3%)	None (38.5%), Moderate (23.1%), Very high (21.6%), Scattered/few (16.9%)
Tuber shape	Round (50%), Oval (50%)	Cylindrical (66.7%), Oval oblong (33.3%)	Oval oblong (39.8%), Cylindrical (25.4%), Oval (24.9%), Round (6.24%), Flattened (3.7%)
Bulbil formation	None (100%)	None (50%), Low (33.3%), High (16.7%)	None (50.1%), Low (29.1%), High (11.6%), Moderate 99.2%)
Tuber oxidation	No oxidation (100%)	Slow/slight oxidation (100%)	No oxidation (60.7%), Slow/slight oxidation (34.8%), Fast oxidation (4.5%)
Anthracnose min	Slightly Infected (66.7%), healthy (33.3%)	Healthy (100%)	Healthy (90.8%), Slightly Infected (9.2%)
Anthracnose max	Slightly Infected (100%)	Slightly Infected (100%)	Slightly Infected (78.4%), Healthy (19.9%), Highly Infected (1.7%)

sprouted tuber sett and the emergence of a shoot above the ground.

Number of primary vines per plant

This was determined by counting the number of primary vines (stems) produced per plant at 20 days after emergence.

Days to tuber initiation

The bases of the plants were exposed six weeks after planting and inspected for the presence of new tubers every other day until tubers were observed for all the plants. The soil was carefully opened and closed to avoid root damage. The six weeks starting time was chosen based on a previous study (Sartie et al., 2011) in a population of breeding lines and landrace varieties of *D. alata* that showed that tubers were not initiated before 55 days after planting in two consecutive years.

Number of tubers per plant

This was determined by counting the harvested tubers per plant.

Days to flowering

These were counted as the numbers of days between shoot emergence and flowering.

Tuber yield per plant

The weight (kg) of tubers per plant was measured immediately after harvest.

Ploidy levels for all the progeny and parents were determined using a flow cytometer (Obidiegwu et al., 2009).

Statistical methods

For the qualitatively scored traits, the number of setts with results in each of the categories was tallied and converted to a percentage of the total number of setts with values (missing values were not used in the total).

For the quantitatively scored traits, variance components (Robinson, 1987) were calculated using a linear mixed model with random terms for clone, and replication within each clone. The variation among the setts within a plot was used as the residual. Narrow-sense heritability, h^2 was calculated from the variance components in two ways: 1) h^2 = clone / (clone + residual); 2) h^2 = clone / (clone + rep + residual).

Comparisons between the two parental lines (TDa 01/00081 and TDa 87/01091) were performed using a linear mixed model (Patterson and Thompson, 1971) with a fixed term for clone and a random term for replicate, for each of the quantitatively scored variables.

To calculate summary statistics for the progeny, the results (of the three setts) were first averaged for each plot, and then summary statistics (mean, minimum and maximum) were calculated using the averages. The averages were tested for normality using the Anderson-Darling test, and Spearman rank correlations were calculated between the variables.

RESULTS

Qualitatively scored traits

Considerable variation was observed amongst the progeny for all the traits (Table 2). For most of the traits (flowering intensity, tuber shape, bulbil formation, tuber browning and reaction to anthracnose infection), a proportion of the progeny population exhibited a phenotype that was absent in either parents (female TDa 01/00081 and male TDa 87/01091).

Among the plants that flowered, 49% were males and 19.9% females, however more than a quarter of the population (31%) did not flower (Table 2 and Figure 1a). About 45% of progeny population produced flowers moderately, or profusely (Table 2 and Figure 1b). Tuber

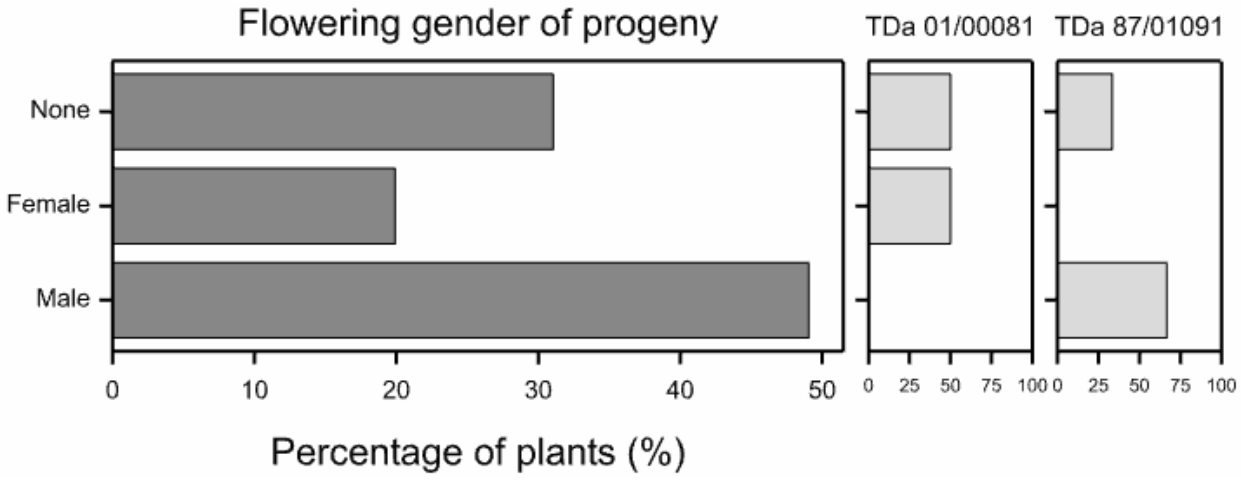

Figure 1a. Flowering and sex of plants that flowered.

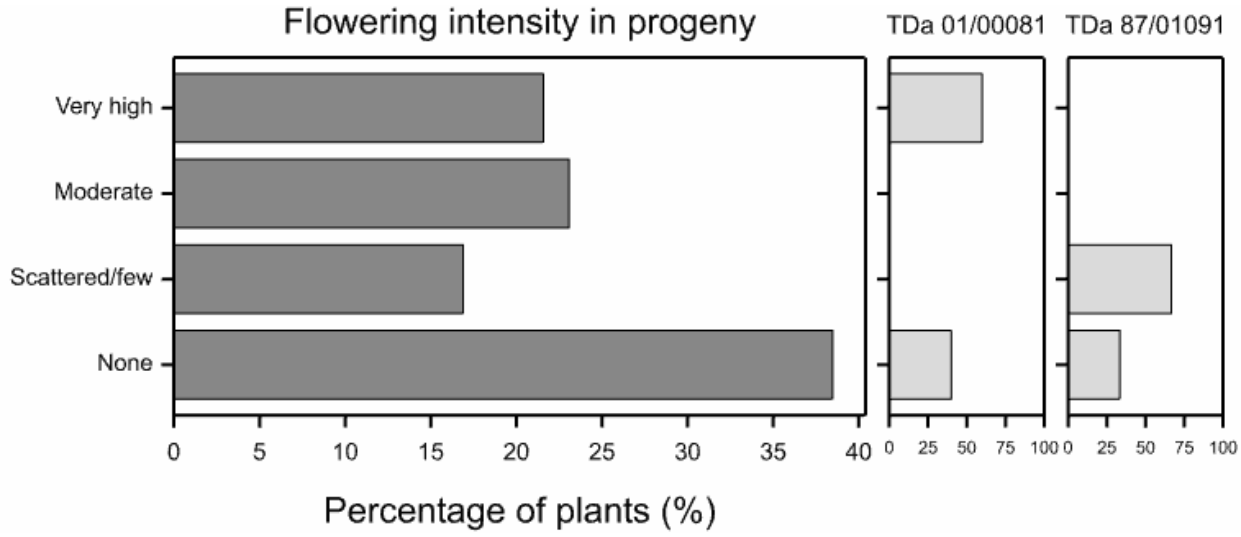

Figure 1b. Percentage of plants from progeny and two parental lines in each flowering intensity category.

shape (Table 2 and Figure 1c) varied the most in the population, with five categories observed. Nearly half of the population did not produce bulbils (Table 2 and Figure 1d), but a reasonable proportion of the progeny (11.6%) produced more than 10 bulbils/plant. Tuber browning is associated with poor eating quality in yam, and the trait segregated in the progeny at three levels with 61% of the population producing tubers that did not turn brown upon exposure of cut surface to the atmosphere (Table 2 and Figure 1e). Assessment based on maximum infection scores shows that only 20% of the genotypes were resistant, or tolerant to anthracnose disease (Table 2 and Figure 1f), as they were either healthy, or had less than 2% symptoms of the disease (Table 1). A small proportion of the progeny (6.6%) produced tubers with short dormancy that sprouted before they were harvested. The parents differed in flowering sex, flowering intensity, tuber shape, bulbil formation and tuber oxidation, (Table 2 and Figure 1), but were similar in levels of anthracnose infection (Figure 1f).

Quantitatively scored traits

Summary statistics for the progeny means for the parents and the results of statistical comparisons between the parents are shown in Table 3. The parents differ significantly ($p < 0.05$) in tubers/plant and primary vines/plant. Histograms of the results for the progeny are shown in Figures 2a to 2f. Although the results of Anderson-Darling tests for normality of the progeny results show that all but one variable, tuber yield/plant, differ significantly from being normally distributed (Table 3), normal probability Q-Q plots of the progeny results (Data not shown) suggest

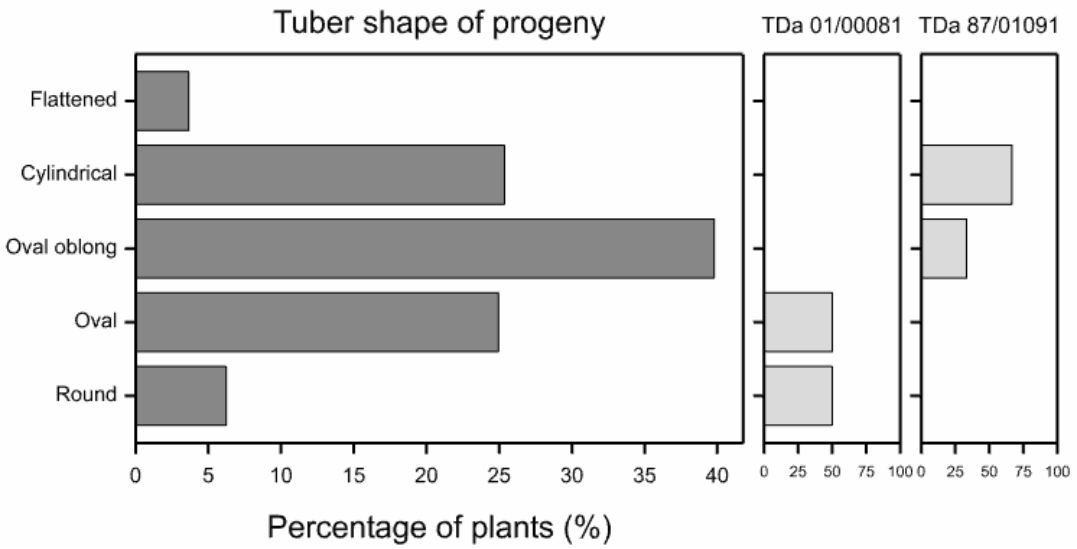

Figure 1c. Percentage of plants from progeny and two parental lines in each tuber shape category.

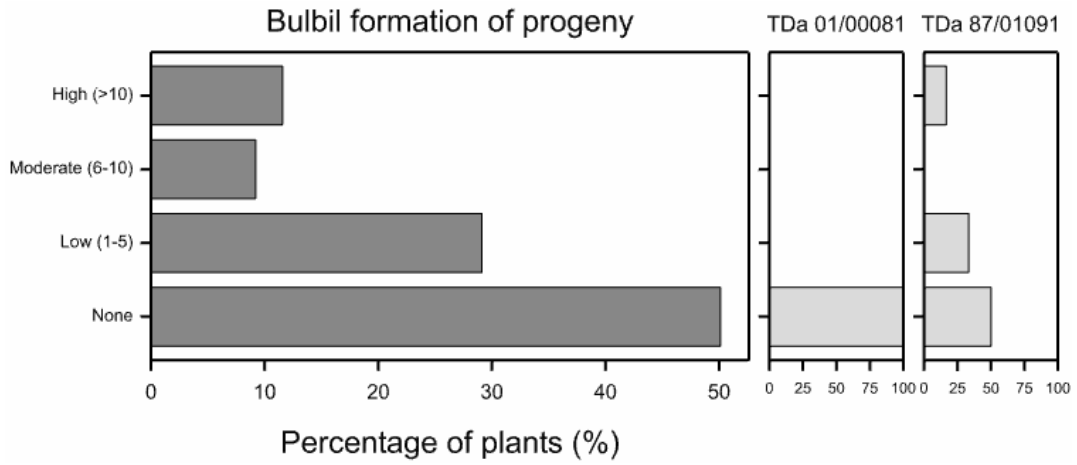

Figure 1d. Percentage of plants from progeny and two parental lines in each bulbil formation category.

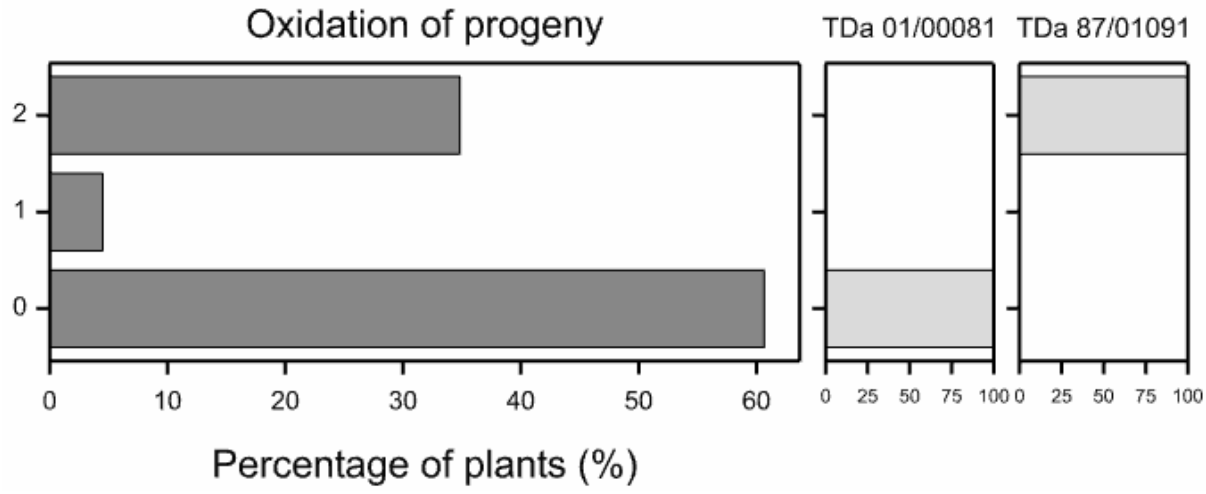

Figure 1e. Percentage of plants from progeny and two parental lines in each oxidation category.

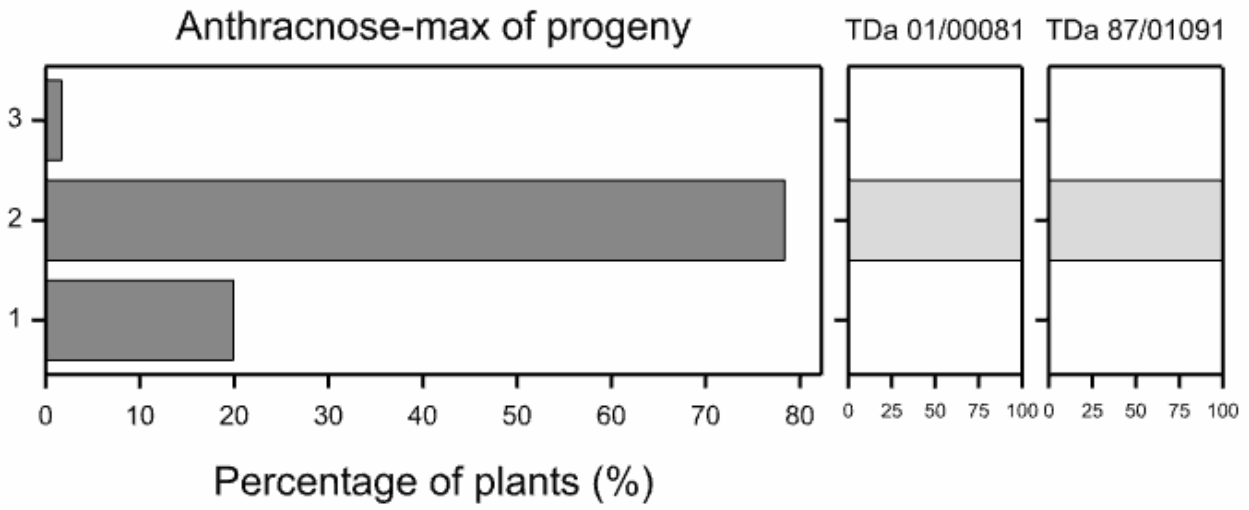

Figure 1f. Percentage of plants from progeny and two parental lines in each anthracnose-maximum category.

Table 3. Summary statistics (mean, minimum, maximum) and normality for quantitative traits assessed in progeny and parents of mapping population AM1 during 2010/2011 yam growing season. P^1 is for comparison of parent means using a linear mixed model. Anderson-Darling *A* tests for normality of quantitative traits measured from progeny. Variables with P-values <0.05 are considered significantly different from normally-distributed.

Quantitatively scored trait	Progeny results			TDa 87/01091	TDa 01/00081	P^1	Normality	
	Mean	Minimum	Maximum	Mean	Mean		*A*	*P*
Days to shoot emergence	19.3	13.0	30.7	22.0	24.3	0.59	0.91	<0.03
Primary vines/plant	5.3	1.3	20.3	3.0	4.2	0.058	8.46	<0.01
Tubers/plant	2.6	1.0	6.0	2.0	2.7	0.025	3.46	<0.01
Days to tuber initiation	82.8	75.0	137.0	80.0	84.5	0.14	6.76	<0.01
Days to flowering	133.9	90.3	154.0	139.5	128.7	n/a	1.46	<0.01
Tuber yield/plant (Kg)	3.6	0.3	7.8	3.3	3.2	0.89	0.49	>0.15

n/a = P-value is not available because one parent had results from only one rep.

Table 4. Spearman rank correlations between quantitatively scored traits assessed in AM1 yam mapping population during 2010/2011 yam growing season. Values in parentheses are p-values.

Quantitatively scored variable	Days to shoot emergence	Number of primary vines/plant	Number of tubers/stand	Days to tuber initiation	Days to flowering after emergence
No. primary vines/plant	-0.27 (0.003)	-			
No. tubers/stand	-0.29 (0.001)	0.54 (<0.001)	-		
Days to tuber initiation	-0.01 (0.95)	-0.08 (0.39)	0.15 (0.10)	-	
Days to flowering after emergence	-0.36 (<0.001)	0.21 (0.021)	0.22 (0.016)	-0.09 (0.31)	-
Tuber yield/stand	-0.10 (0.29)	0.02 (0.79)	0.01 (0.95)	-0.28 (0.002)	0.22 (0.015)

that days to shoot emergence and days to flowering after emergence are not practically different from being normally distributed.

Most of the quantitatively scored traits were only weakly correlated with each other (Table 4). The number of tubers/plant and the number of primary vines/plant were moderately positively correlated (r = 0.54). Tuber yield correlated negatively (p = 0.002) with days to tuber initiation but positively (p = 0.015) with days to flowering.

Days to shoot emergence correlated negatively (p < 0.001) with days to flowering and tuber number/stand replicates of the same clone, and the "residual" component is the variance among the setts within a plot.

When calculating narrow-sense heritability, the "rep"

Table 5. Variance components and narrow-sense heritability for quantitative traits assessed in mapping population AM1 in 2010/2011 yam growing season. The narrow-sense heritability was calculated using the variance components in two ways: h^2 = clone / (clone + residual); and h^2 = clone / (clone + rep + residual).

Quantitative Trait	Variance component			Narrow-sense heritability	
	Clone	Rep	Residual	h^2	h^2
Days to shoot emergence	0.200	0.00001	30.141	0.007	0.007
No. primary vines/plant	8.567	0.437	4.907	0.636	0.616
No. tubers/stand	0.697	0.000	1.655	0.296	0.296
Days to tuber initiation	23.167	23.167	12.494	0.650	0.394
Days to flowering after emergence	35.654	30.599	74.289	0.324	0.254
Tuber yield/stand	1.316	0.199	1.617	0.449	0.420

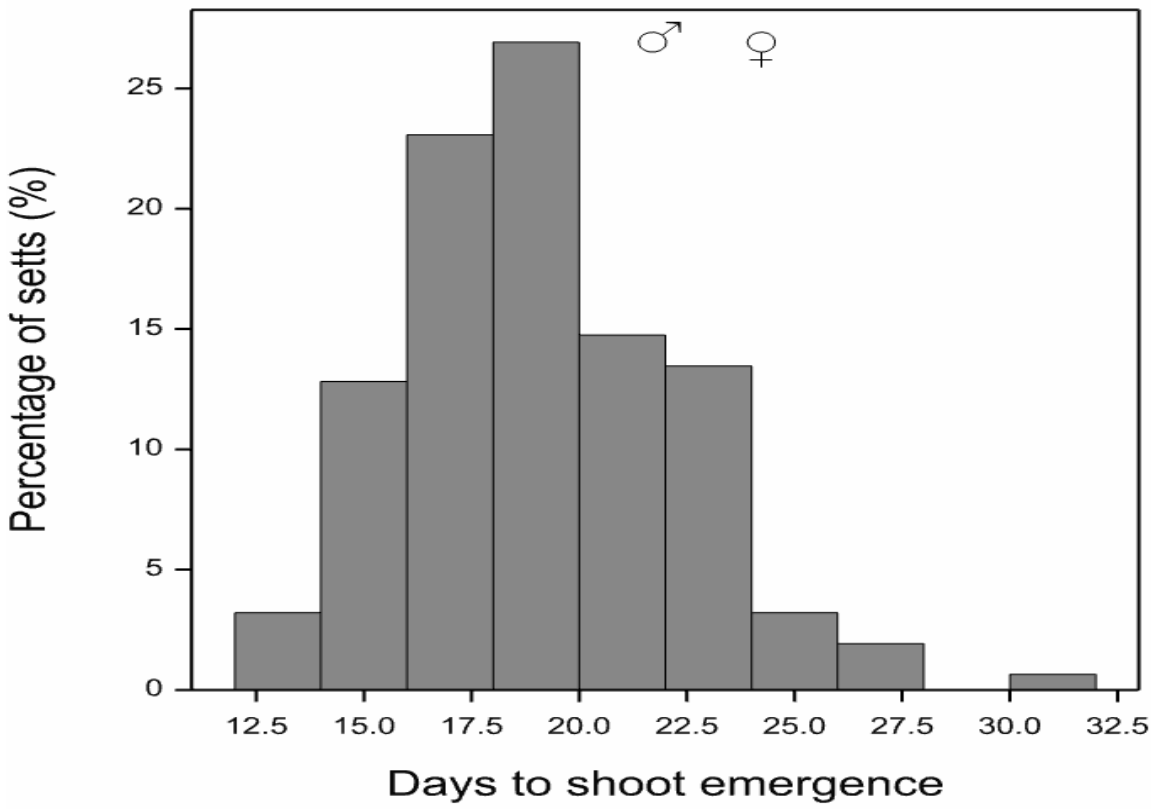

Figure 2a. Histogram of days to shoot emergence results from all progeny and the two parents (♀ = female parent and ♂ = male parent).

variance can either be included in the total variance (the denominator of the fraction) or not. Heritability was calculated in both ways (Table 5), and was moderately high for most of the traits, but very low for days to shoot emergence.

Ploidy analysis

Ploidy analysis results show that two of the progeny had ploidy levels of 2n = 80 (8x), while the rest, including their parents, had 2n = 40 (4x). The two 8x genotypes, both males, did not express a phenotype significantly different from the other genotypes.

DISCUSSION

Considerable variation was observed among the progeny for the 12 traits that were assessed. Earlier results have shown the segregation of parental alleles in population AM1 when DNA of six selected progenies and the two

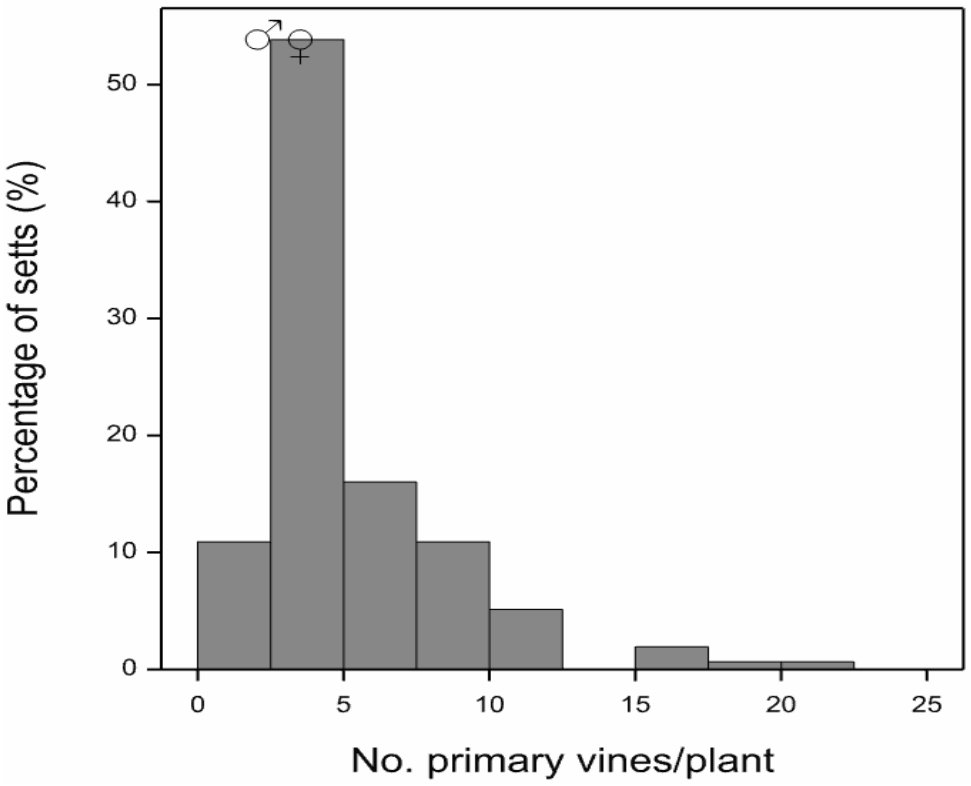

Figure 2b. Histogram of results from all progeny and the two parents for number of primary vines per plant (♀ = female parent and ♂ = male parent).

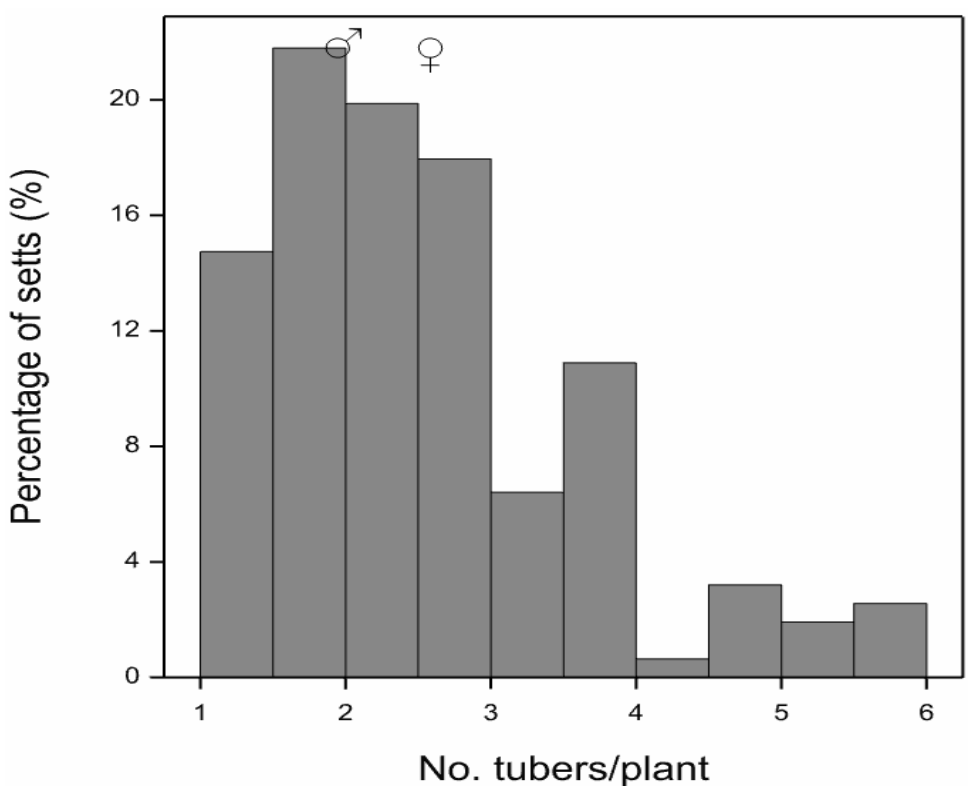

Figure 2c. Histogram of results from all progeny and the two parents for number of tubers per stand (♀ = female parent and ♂ = male parent).

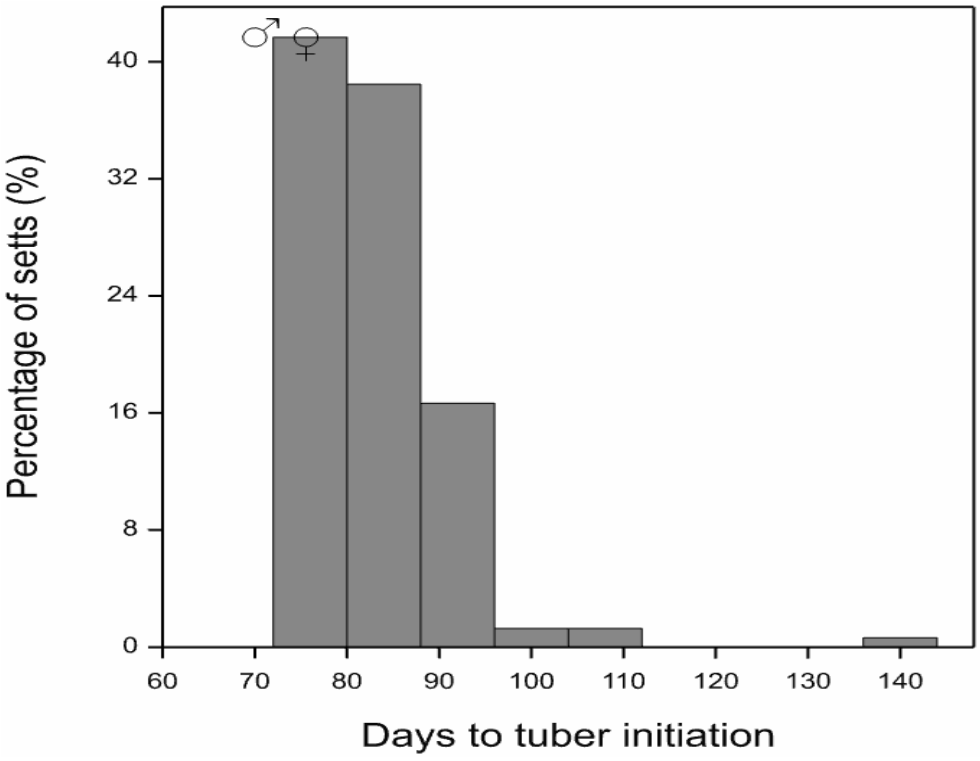

Figure 2d. Histogram of results from all progeny and the two parents for days to tuber initiation (♀ = female parent and ♂ = male parent).

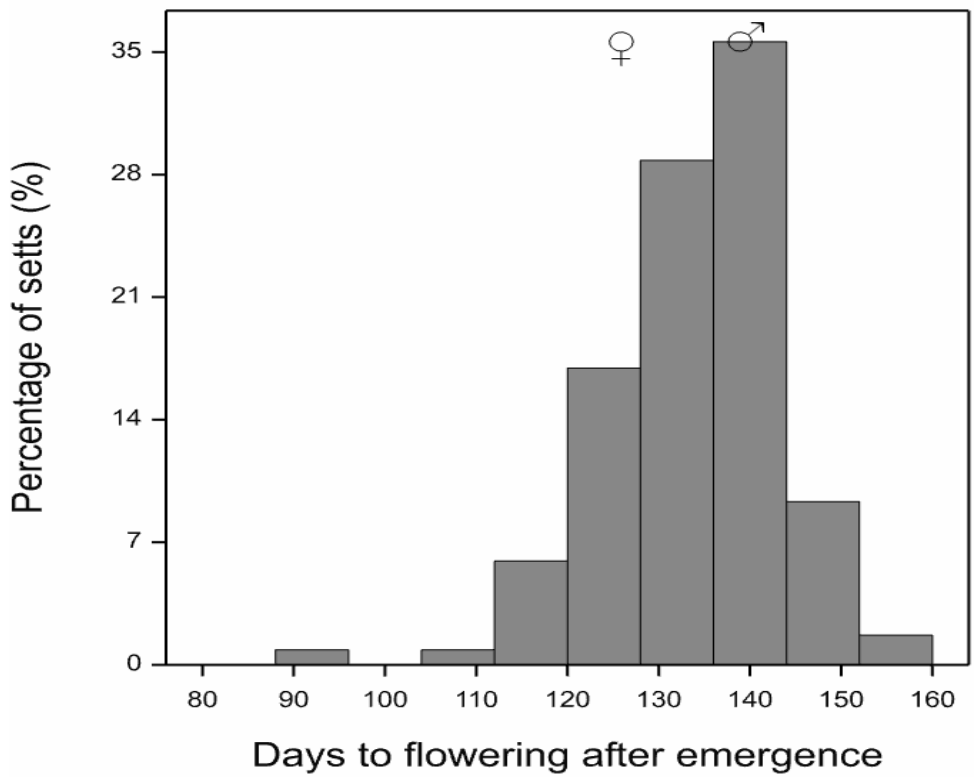

Figure 2e. Histogram of results from all progeny and the two parents for number of days to flowering after emergence (♀ = female parent and ♂ = male parent).

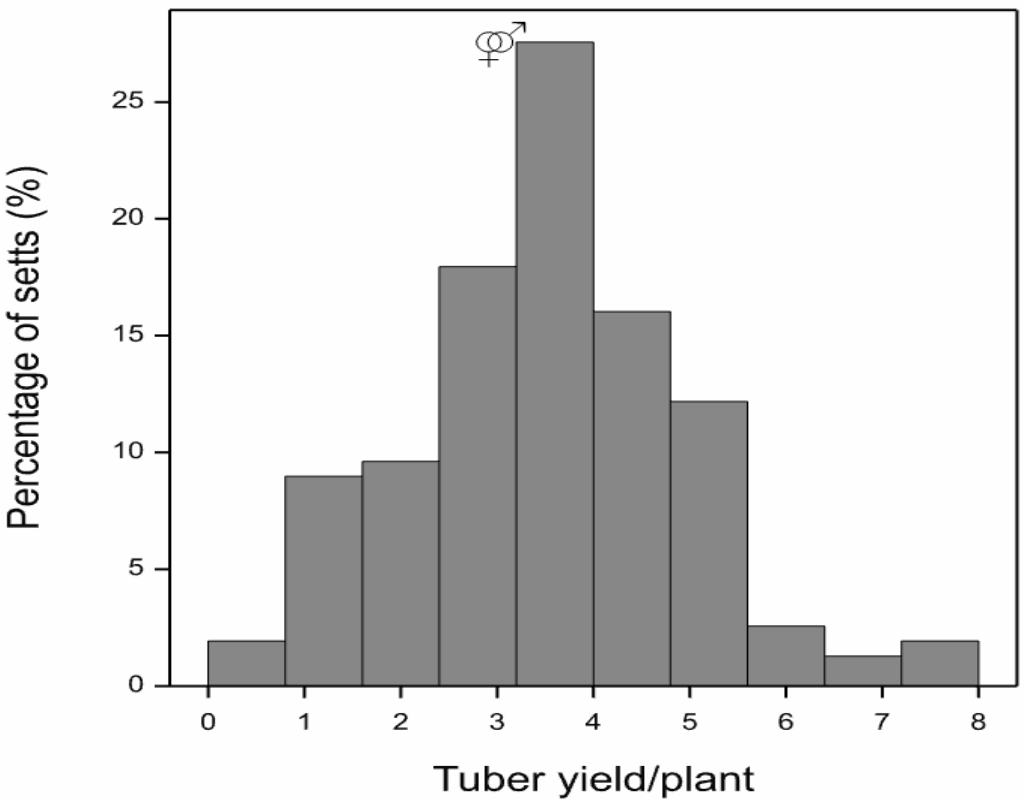

Figure 2f. Histogram of results from all progeny and the two parents for tuber yield per stand (♀ = female parent and ♂ = male parent).

parents were analysed with SSR markers (Sartie and Asiedu, 2011). The findings taken together indicate that population AM1 should be suitable for genetic mapping and development of markers linked to these traits in *D. alata*. Transgressive segregation (the production of extreme phenotypes in the progeny compared to the parental lines) that was observed for some of the traits (flowering intensity, tuber shape, bulbil formation, tuber oxidation and reaction to anthracnose disease), represents a potential source of novel genetic variation in hybrids that may be significant for the genetic improvement in these traits (de Vicente and Tanksley, 1993). Correlation analysis shows a weak association among most of the traits, which suggest that they are largely independent of one another, except for tuber yield-related traits that were shown to be moderately correlated. As the current investigation was conducted for only one year in a partial population of 78 out of 144 progeny of mapping population AM1, it is highly desirable that these preliminary results are validated in the whole population over two years, before genetic mapping proceeds.

Tuber yield- related traits in *D. alata* had been previously identified as shoot dry weight and time of shoot emergence, with tuber yield correlating positively with shoot dry weight, but negatively with time of shoot emergence (Sartie et al., 2011). Days to flowering was not assessed in the previous study, while shoot dry weight was not investigated in the current study. The previous study was undertaken in a smaller population of eight *D. alata* accessions of cultivars. Results based on findings of the current and previous (Sartie et al., 2011) studies in two populations of different genetic backgrounds, indicate that tuber yield-related traits in *D. alata* include: number of primary vines/plant; days to shoot emergence; shoot dry weight; days to tuber initiation; and days to flowering. Days to tuber initiation and shoot emergence correlated negatively with tuber fresh weight in both studies, indicating that delayed shoot emergence or tuber initiation may result in low tuber yield. Moreover, the low heritability of days to shoot emergence suggests that this trait may be largely influenced by the environment.

Extent of flowering affects the ease and success of developing breeding and mapping populations in yam. Some genotypes do not flower, or they flower only sparingly. Extent of flowering may also be affected by the environment, such as season and location (Hamadina et al., 2009). In the current study, more than a quarter of the population (31%) did not flower (Table 2 and Figure 1a), and their sex could not be determined. This poses a challenge for developing hybrid populations in *D. alata*. Assessment of population AM1 for flowering at multi-locations and across seasons or years will be useful for

the identification of genotypes that flower every year, or only seasonally.

Tuber shape is an important trait for marketing and exporting of yam tubers. Variable tuber shapes including round, oval, oval oblong, cylindrical and flattened segregated in the study population (Table 2 and Figure 1c), which indicates that population AM1 can be used for developing cultivars of specific shapes. Tuber shape, however, can be manipulated artificially, as some farmers manage the process of changing the form by adjusting the type of the mounds, while others have introduced flat stones into the mounds to produce short and fat tubers (Zannou et al., 2006).

The availability of seed tubers for planting is a major limitation in yam production, due to low seed multiplication factor of the crop, on one hand, and that the tuber is the edible part used as food, on the other hand. Bulbils are aerial tubers that can be used as seeds in crop production. About 40% of genotypes in the study population produced bulbils (Table 2 and Figure 1d), which would serve as complementary source of seed tubers. The segregation of bulbil formation in this population therefore confirms the suitability of population AM1 for genetic analysis and marker development for bulbil formation in *D. alata*. Phenotypic expression for bulbil production suggests that the trait may be influenced by environment, as shown in the parent that produced bulbils.

Tuber browning (discoloration of yam when a cut surface turns brown on exposure to air), which is associated with poor eating quality is a problem in *D. alata* (Martin and Ruberte, 1976). In this study, 61% of the genotypes in mapping population AM1 produced tubers that were non-browning, while the others were associated with fast or slow browning (Table 2 and Figure 1e). Population AM1 is therefore a potential gene pool for breeding for non-browning combined with other desirable traits in *D. alata* and it would also be suitable for genetic analysis and marker development for tuber browning in *D. alata*.

Anthracnose is a major disease that affects the production of *D. alata*, with the symptoms of this disease visible on the leaves of infected plants. Evaluating a yam plant for disease incidence on the field requires scoring for both minimum and maximum infection, due to the often non-uniform distribution of disease in field plots.

Ideally highly resistant clones are expected to have relatively low to moderate scores even for the maximum infection reading. Trying to give an average reading by just looking at the field will not capture the potential maximum severity the clone could suffer when under intense pressure. This indicates that phenotyping anthracnose disease based on natural infection on the field is difficult and sometimes misleading. Phenotyping of this disease could be more reliable following inoculation of plants under controlled conditions as reported previously for *D. alata* (Mignouna et al., 2001) and for other diseases in other crops, for example *Pseudomonas syringae* pv. *actinidae* (*Psa*) in Kiwifruit (*Actinidia* sp.) (Gardiner et al., 2013) and Blast (*Magnaporthe oryzae* (Hebert) Barr.) and Bacterial leaf blight (*Xanthomonas oryzae* pv. oryzae (*Xoo*) of rice (*Oryza* sp.) (Pinta et al., 2013). Our result shows that some genotypes of the study population were resistant, or tolerant to anthracnose infection, whilst neither of their parents showed complete resistance (Table 2 and Figure 1f). This indicates that although population AM1 might not be best suited for mapping markers for resistance, it may be a beneficial gene pool to facilitate genetic improvement for anthracnose resistance in this species.

Long tuber dormancy (which may last over 4 months), coupled with a long growth and development period of about 7 months (Sartie et al., 2011), prevents the production of *D. alata* more than once or twice in a year, which hinders fast improvement and increased production of the crop. A small proportion (about 7%) of population AM1 had their tubers sprouted before they were harvested, which indicates the possibility of double cultivation of those genotypes with short dormancy, or using them as parents for developing cultivars for multiple production within a year, providing that the other growth factors are available. However, short tuber dormancy would mean short tuber shelf-life, which may reduce consumer preference.

Good cooking quality is a valuable characteristic in cultivar development in yam. Parents of mapping population AM1 differ on cooking quality (Sartie and Asiedu, 2011), with a possibility for the trait to segregate in the population. However, as cooking quality was not assessed in the current investigation, it would be necessary to evaluate population AM1 for this trait in future studies.

D. alata includes varieties with three ploidy levels of 2n = 40, 60 and 80 chromosomes, which have been previously classified as tetraploid, hexaploid and octaploid respectively, with x = 10 as basic chromosome number (Abraham and Nair, 1991; Gamiette et al., 1999; Malapa et al., 2005; Obidiegwu et al., 2009). However, genetic analysis with Amplified Fragment Length Polymorphic (AFLP) markers in F_1 hybrids of *D. alata* revealed that the markers segregated as in a diploid cross-pollinated population (Mignouna et al., 2002). A recent review on ploidy status of *D. alata* using cytogenetics as well as SSR markers (Arnau et al., 2009) has also established that plants with 2n = 40 chromosomes are diploids with the basic chromosome number of x = 20. In the current study, most (97%) of the progeny were 2n = 40 as were their parents, indicating that mapping population AM1 is a diploid population derived from diploid parents.

Conclusions

Mapping population AM1 is a valuable resource for QTL mapping and genetic marker development for marker-assisted breeding for tuber yield, tuber shape, bulbil formation, tuber browning and flowering intensity in water

yam (*D. alata)*. There were considerable phenotypic variations amongst the progeny for all the assessed traits, with some progeny showing extreme phenotypes that were not expressed in the parents. Ploidy analysis indicated that mapping population AM1 is a diploid population derived from diploid parents.

Conflict of Interests

The author(s) have not declared any conflict of interests.

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